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SEQUENCE LISTING

<110> Droux, Michel  
DeRose, Richard  
Job, Dominique

<120> Method for Increasing the Content of Sulphur Compounds  
and In Particular of Cysteine, Methionine and  
Glutathione in Plants and Plants Obtained

<130> 5500\*42

<140> 09/486,334

<141> 2001-07-11

<160> 23

<170> PatentIn Ver. 2.0

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Arg Thr Gly Asn Thr Gln Asp Asp Asp Ser Arg Phe Cys Cys Ile Lys  
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75 80 85	
tcc gta aag ctc agc aat tta aac cta cca agc aac aca ctc ttc gaa	342
Ser Val Lys Leu Ser Asn Leu Asn Leu Pro Ser Asn Thr Leu Phe Glu	
90 95 100	
ctg ttc ata agc gtt tta gaa gaa agc cct gag atc atc gaa tcc acg	390
Leu Phe Ile Ser Val Leu Glu Glu Ser Pro Glu Ile Ile Glu Ser Thr	
105 110 115 120	
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Lys Gln Asp Leu Ile Ala Val Lys Glu Arg Asp Pro Ala Cys Ile Ser	
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Tyr Val His Cys Phe Leu Gly Phe Lys Gly Phe Leu Ala Cys Gln Ala	
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Leu Leu Ile Gln Asn Arg Val Ser Glu Ser Phe Ala Val Asp Ile His	
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Pro Gly Ala Lys Ile Gly Lys Gly Ile Leu Leu Asp His Ala Thr Gly	
185 190 195 200	
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Val Val Ile Gly Glu Thr Ala Val Val Gly Asp Asn Val Ser Ile Leu	
205 210 215	
cac gga gtg acc ttg gga gga aca ggg aaa cag agt ggt gat cgg cat	726
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Pro Lys Ile Gly Asp Gly Val Leu Ile Gly Ala Gly Ser Cys Ile Leu	
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 Arg Leu Ile Gly Gly Lys Glu Asn Pro Arg Lys His Asp Lys Ile Pro  
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tgt ctg act atg gac cag aca tcg tat tta acc gag tgg tct gat tat 966  
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 35 40 45

Trp Ile Lys Met Leu Glu Glu Ala Lys Ser Asp Val Lys Gln Glu Pro  
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Ile Leu Ser Asn Tyr Tyr Tyr Ala Ser Ile Thr Ser His Arg Ser Leu  
 65 70 75 80

Glu Ser Ala Leu Ala His Ile Leu Ser Val Lys Leu Ser Asn Leu Asn  
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Leu Pro Ser Asn Thr Leu Phe Glu Leu Phe Ile Ser Val Leu Glu Glu  
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Ser Pro Glu Ile Ile Glu Ser Thr Lys Gln Asp Leu Ile Ala Val Lys  
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Glu Arg Asp Pro Ala Cys Ile Ser Tyr Val His Cys Phe Leu Gly Phe

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Lys Gln Asn Arg Lys Ile Val Ala Leu Leu Ile Gln Asn Arg Val Ser		
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Glu Ser Phe Ala Val Asp Ile His Pro Gly Ala Lys Ile Gly Lys Gly		
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Ile Leu Leu Asp His Ala Thr Gly Val Val Ile Gly Glu Thr Ala Val		
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Val Gly Asp Asn Val Ser Ile Leu His Gly Val Thr Leu Gly Gly Thr		
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225	230	235 240
Ile Gly Ala Gly Ser Cys Ile Leu Gly Asn Ile Thr Ile Gly Glu Gly		
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Ala Lys Ile Gly Ser Gly Ser Val Val Val Lys Asp Val Pro Ala Arg		
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Thr Thr Ala Val Gly Asn Pro Ala Arg Leu Ile Gly Gly Lys Glu Asn		
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 Glu Ala Glu Ala Ala Ser Ala Ala Ile Ser Ala Ala Ala Asp Ala  
 25 30 35 40

gaa gct gcc gga tta tgg aca cag atc aag gcg gaa gct cgc cgt gat 198  
 Glu Ala Ala Gly Leu Trp Thr Gln Ile Lys Ala Glu Ala Arg Arg Asp  
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gct gag gcg gag cca gct tta gct agc tat cta tat tcg acg att ctt 246  
 Ala Glu Ala Glu Pro Ala Leu Ala Ser Tyr Leu Tyr Ser Thr Ile Leu  
 60 65 70

tct cat tcg tct ctt gaa cga tct atc tcg ttt cat cta gga aac aag 294  
 Ser His Ser Ser Leu Glu Arg Ser Ile Ser Phe His Leu Gly Asn Lys  
 75 80 85

ctt tgt tcc tca acg ctt tta tcc aca ctt tta tac gat ctg ttc tta 342  
 Leu Cys Ser Ser Thr Leu Leu Ser Thr Leu Leu Tyr Asp Leu Phe Leu  
 90 95 100

aac act ttt tcc tcc gat cct tct ctt cgt aac gcc acc gtc gca gat 390  
 Asn Thr Phe Ser Ser Asp Pro Ser Leu Arg Asn Ala Thr Val Ala Asp  
 105 110 115 120

cta cgc gct gct cgt gtt cgt gat cct gct tgt atc tcg ttc tct cat 438  
 Leu Arg Ala Ala Arg Val Arg Asp Pro Ala Cys Ile Ser Phe Ser His  
 125 130 135

tgt ctc ctc aat tac aaa ggc ttc tta gct att cag gcg cat cgt gta 486  
 Cys Leu Leu Asn Tyr Lys Gly Phe Leu Ala Ile Gln Ala His Arg Val  
 140 145 150

tca cac aag cta tgg aca caa tca cgg aag cca tta gca tta gct cta 534  
 Ser His Lys Leu Trp Thr Gln Ser Arg Lys Pro Leu Ala Leu Ala Leu  
 155 160 165

cac tca aga atc tcc gat gta ttc gct gtt gat atc cat cca gca gcg 582  
 His Ser Arg Ile Ser Asp Val Phe Ala Val Asp Ile His Pro Ala Ala  
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 Lys Ile Gly Lys Gly Ile Leu Leu Asp His Ala Thr Gly Val Val Val

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205	210	215		
aca cta ggt gga aca ggt aaa gct tgt gga gat aga cat ccg aag atc				726
Thr Leu Gly Gly Thr Gly Lys Ala Cys Gly Asp Arg His Pro Lys Ile				
220	225	230		
ggt gac ggt tgt ttg att gga gct gga gcg act att ctt gga aat gtg				774
Gly Asp Gly Cys Leu Ile Gly Ala Gly Ala Thr Ile Leu Gly Asn Val				
235	240	245		
aag att ggt gca ggt gct aaa gta gga gct ggt tct gtt gtg ctg att				822
Lys Ile Gly Ala Gly Ala Lys Val Gly Ala Gly Ser Val Val Leu Ile				
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Thr Leu Leu Tyr Asp Leu Phe Leu Asn Thr Phe Ser Ser Asp Pro Ser  
 100 105 110

Leu Arg Asn Ala Thr Val Ala Asp Leu Arg Ala Ala Arg Val Arg Asp  
 115 120 125

Pro Ala Cys Ile Ser Phe Ser His Cys Leu Leu Asn Tyr Lys Gly Phe  
 130 135 140

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 145 150 155 160

Arg Lys Pro Leu Ala Leu Ala Leu His Ser Arg Ile Ser Asp Val Phe  
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Ala Val Asp Ile His Pro Ala Ala Lys Ile Gly Lys Gly Ile Leu Leu  
 180 185 190

Asp His Ala Thr Gly Val Val Val Gly Glu Thr Ala Val Ile Gly Asn  
 195 200 205

Asn Val Ser Ile Leu His His Val Thr Leu Gly Gly Thr Gly Lys Ala  
 210 215 220

Cys Gly Asp Arg His Pro Lys Ile Gly Asp Gly Cys Leu Ile Gly Ala  
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 245 250 255

Gly Ala Gly Ser Val Val Leu Ile Asp Val Pro Cys Arg Gly Thr Ala  
 260 265 270

Val Gly Asn Pro Ala Arg Leu Val Gly Gly Lys Glu Lys Pro Thr Ile  
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Arg Thr Gly Lys Pro Gln Ile Ser Pro Arg Asp Ser Ser Lys His His  
10 15 20

gac gat gaa tct ggc ttt cgt tac atg aac tac ttc cgt tat cct gat 150  
Asp Asp Glu Ser Gly Phe Arg Tyr Met Asn Tyr Phe Arg Tyr Pro Asp  
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cga tct tcc ttc aat gga acc cag acc aaa acc ctc cat act cgt cct 198  
Arg Ser Ser Phe Asn Gly Thr Gln Thr Lys Thr Leu His Thr Arg Pro  
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ttg ctt gaa gat ctc gat cgc gac gct gaa gtc gat gat gtt tgg gcc 246  
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aaa atc cga gaa gag gct aaa tct gat atc gcc aaa gaa cct att gtt 294  
Lys Ile Arg Glu Glu Ala Lys Ser Asp Ile Ala Lys Glu Pro Ile Val  
75 80 85

tcc gct tat tat cac gct tcg att gtt tct cag cgt tcg ttg gaa gct 342  
Ser Ala Tyr Tyr His Ala Ser Ile Val Ser Gln Arg Ser Leu Glu Ala  
90 95 100

gcg ttg gcg aat act tta tct gtt aaa ctc agc aat ttg aat ctt cca 390  
Ala Leu Ala Asn Thr Leu Ser Val Lys Leu Ser Asn Leu Asn Leu Pro  
105 110 115 120

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Asp Pro Ala Cys Ile Ser Tyr Val His Cys Phe Leu His Phe Lys Gly			
155	160	165	
ttc ctc gct tgt caa gcg cat cgt att gct cat gag ctt tgg act cag	582		
Phe Leu Ala Cys Gln Ala His Arg Ile Ala His Glu Leu Trp Thr Gln			
170	175	180	
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185	190	195	200
ttc gct gtt gat ttc cac cct gga gct aaa atc ggt acc ggg att ttg	678		
Phe Ala Val Asp Phe His Pro Gly Ala Lys Ile Gly Thr Gly Ile Leu			
205	210	215	
cta gac cat gct acg gct att gtg atc ggt gag acg gcg gtt gtg ggg	726		
Leu Asp His Ala Thr Ala Ile Val Ile Gly Glu Thr Ala Val Val Gly			
220	225	230	
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Asn Asn Val Ser Ile Leu His Asn Val Thr Leu Gly Gly Thr Gly Lys			
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265	270	275	280
att ggt gcg ggg tcg gtg gtg ttg aaa gac gtg ccg ccg cgt acg acg	918		
Ile Gly Ala Gly Ser Val Val Leu Lys Asp Val Pro Pro Arg Thr Thr			
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315

320

325

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1048

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&lt;400&gt; 6

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Met Asn Tyr Phe Arg Tyr Pro Asp Arg Ser Ser Phe Asn Gly Thr Gln

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Thr Lys Thr Leu His Thr Arg Pro Leu Leu Glu Asp Leu Asp Arg Asp

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Ala Glu Val Asp Asp Val Trp Ala Lys Ile Arg Glu Glu Ala Lys Ser

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80

Asp Ile Ala Lys Glu Pro Ile Val Ser Ala Tyr Tyr His Ala Ser Ile

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90

95

Val Ser Gln Arg Ser Leu Glu Ala Ala Leu Ala Asn Thr Leu Ser Val

100

105

110

Lys Leu Ser Asn Leu Asn Leu Pro Ser Asn Thr Leu Phe Asp Leu Phe

115

120

125

Ser Gly Val Leu Gln Gly Asn Pro Asp Ile Val Glu Ser Val Lys Leu

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135

140

Asp Leu Leu Ala Val Lys Glu Arg Asp Pro Ala Cys Ile Ser Tyr Val

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155

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His Cys Phe Leu His Phe Lys Gly Phe Leu Ala Cys Gln Ala His Arg

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Ile Ala His Glu Leu Trp Thr Gln Asp Arg Lys Ile Leu Ala Leu Leu

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 225 230 235 240  
 Val Thr Leu Gly Gly Thr Gly Lys Gln Cys Gly Asp Arg His Pro Lys  
 245 250 255  
 Ile Gly Asp Gly Val Leu Ile Gly Ala Gly Thr Cys Ile Leu Gly Asn  
 260 265 270  
 Ile Thr Ile Gly Glu Gly Ala Lys Ile Gly Ala Gly Ser Val Val Leu  
 275 280 285  
 Lys Asp Val Pro Pro Arg Thr Thr Ala Val Gly Asn Pro Ala Arg Leu  
 290 295 300  
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His Phe Thr Met Ser Leu Tyr Met Leu Arg Ser Ser Ser Pro His Ile	
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25 30 35 40	
cac cat act tta tct cct cct cct tct cct cct cct cct cct atg	198
His His Thr Leu Ser Pro Pro Pro Ser Pro Pro Pro Pro Pro Met	
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Ala Ala Cys Ile Asp Thr Cys Arg Thr Gly Lys Pro Gln Ile Ser Pro	
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Glu Val Asp Asp Val Trp Ala Lys Ile Arg Glu Glu Ala Lys Ser Asp	
125 130 135	
atc gcc aaa gaa cct att gtt tcc gct tat tat cac gct tcg att gtt	486
Ile Ala Lys Glu Pro Ile Val Ser Ala Tyr Tyr His Ala Ser Ile Val	
140 145 150	
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Ser Gln Arg Ser Leu Glu Ala Ala Leu Ala Asn Thr Leu Ser Val Lys	
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Gly Val Leu Gln Gly Asn Pro Asp Ile Val Glu Ser Val Lys Leu Asp	
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Leu Leu Ala Val Lys Glu Arg Asp Pro Ala Cys Ile Ser Tyr Val His	
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Cys Phe Leu His Phe Lys Gly Phe Leu Ala Cys Gln Ala His Arg Ile	
220	225 230
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Ala His Glu Leu Trp Thr Gln Asp Arg Lys Ile Leu Ala Leu Leu Ile	
235	240 245
cag aac aga gtc tct gaa gcc ttc gct gtt gat ttc cac cct gga gct	822
Gln Asn Arg Val Ser Glu Ala Phe Ala Val Asp Phe His Pro Gly Ala	
250	255 260
aaa atc ggt acc ggg att ttg cta gac cat gct acg gct att gtg atc	870
Lys Ile Gly Thr Gly Ile Leu Leu Asp His Ala Thr Ala Ile Val Ile	
265	270 275 280
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Gly Glu Thr Ala Val Val Gly Asn Asn Val Ser Ile Leu His Asn Val	
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acg ctt gga gga acg ggg aaa cag tgt gga gat agg cac ccg aag att	966
Thr Leu Gly Gly Thr Gly Lys Gln Cys Gly Asp Arg His Pro Lys Ile	
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ggc gat ggg gtt ttg att gga gct ggg act tgt att ttg ggg aat atc	1014
Gly Asp Gly Val Leu Ile Gly Ala Gly Thr Cys Ile Leu Gly Asn Ile	
315	320 325
acg att ggt gaa gga gct aag att ggt gcg ggg tcg gtg gtg ttg aaa	1062
Thr Ile Gly Glu Gly Ala Lys Ile Gly Ala Gly Ser Val Val Leu Lys	
330	335 340
gac gtg ccg ccg cgt acg acg gct gtt gga aat ccg gcg agg ttg ctt	1110
Asp Val Pro Pro Arg Thr Thr Ala Val Gly Asn Pro Ala Arg Leu Leu	
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Ser Phe Val Ser Ser Lys Phe Lys His His Thr Leu Ser Pro Pro Pro  
35 40 45

Ser Pro Pro Pro Pro Pro Pro Met Ala Ala Cys Ile Asp Thr Cys Arg  
50 55 60

Thr Gly Lys Pro Gln Ile Ser Pro Arg Asp Ser Ser Lys His His Asp  
65 70 75 80

Asp Glu Ser Gly Phe Arg Tyr Met Asn Tyr Phe Arg Tyr Pro Asp Arg  
85 90 95

Ser Ser Phe Asn Gly Thr Gln Thr Lys Thr Leu His Thr Arg Pro Leu  
100 105 110

Leu Glu Asp Leu Asp Arg Asp Ala Glu Val Asp Asp Val Trp Ala Lys  
115 120 125

Ile Arg Glu Glu Ala Lys Ser Asp Ile Ala Lys Glu Pro Ile Val Ser  
130 135 140

Ala Tyr Tyr His Ala Ser Ile Val Ser Gln Arg Ser Leu Glu Ala Ala  
145 150 155 160

Leu Ala Asn Thr Leu Ser Val Lys Leu Ser Asn Leu Asn Leu Pro Ser  
165 170 175

Asn Thr Leu Phe Asp Leu Phe Ser Gly Val Leu Gln Gly Asn Pro Asp  
180 185 190

Ile Val Glu Ser Val Lys Leu Asp Leu Leu Ala Val Lys Glu Arg Asp  
195 200 205

Pro Ala Cys Ile Ser Tyr Val His Cys Phe Leu His Phe Lys Gly Phe

210	215	220
Leu Ala Cys Gln Ala His Arg Ile Ala His Glu Leu Trp Thr Gln Asp		
225	230	235 240
Arg Lys Ile Leu Ala Leu Leu Ile Gln Asn Arg Val Ser Glu Ala Phe		
	245	250 255
Ala Val Asp Phe His Pro Gly Ala Lys Ile Gly Thr Gly Ile Leu Leu		
	260	265 270
Asp His Ala Thr Ala Ile Val Ile Gly Glu Thr Ala Val Val Gly Asn		
	275	280 285
Asn Val Ser Ile Leu His Asn Val Thr Leu Gly Gly Thr Gly Lys Gln		
	290	300 305
Cys Gly Asp Arg His Pro Lys Ile Gly Asp Gly Val Leu Ile Gly Ala		
305	310	315 320
Gly Thr Cys Ile Leu Gly Asn Ile Thr Ile Gly Glu Gly Ala Lys Ile		
	325	330 335
Gly Ala Gly Ser Val Val Leu Lys Asp Val Pro Pro Arg Thr Thr Ala		
	340	345 350
Val Gly Asn Pro Ala Arg Leu Leu Gly Gly Lys Asp Asn Pro Lys Thr		
	355	360 365
His Asp Lys Ile Pro Gly Leu Thr Met Asp Gln Thr Ser His Ile Ser		
	370	375 380
Glu Trp Ser Asp Tyr Val Ile		
385	390	

<210> 9  
 <211> 1080  
 <212> DNA  
 <213> Arabidopsis thaliana

<220>  
 <221> CDS  
 <222> (1)..(1080)

<220>  
 <221> transit\_peptide  
 <222> (1)..(96)

<400> 9

atg gtg gat cta tct tcc ttt agc ctc ctt ttt gct ttc tcc gtc tct	48
Met Val Asp Leu Ser Ser Phe Ser Leu Leu Phe Ala Phe Ser Val Ser	
1 5 10 15	
ctc tct ttt gtc caa tca aaa aga gtt tgt gat tct tct tta tcg tct	96
Leu Ser Phe Val Gln Ser Lys Arg Val Cys Asp Ser Ser Leu Ser Ser	
20 25 30	
cct tgg aga gat atg aat ggc gat gag ctt cct ttc gag agt ggt ttc	144
Pro Trp Arg Asp Met Asn Gly Asp Glu Leu Pro Phe Glu Ser Gly Phe	
35 40 45	
gag gtt tac gct aag gga act cat aag tca gag ttt gac tcg aat ttg	192
Glu Val Tyr Ala Lys Gly Thr His Lys Ser Glu Phe Asp Ser Asn Leu	
50 55 60	
ctt gat cct cgt tct gat cct att tgg gat gct ata aga gaa gaa gct	240
Leu Asp Pro Arg Ser Asp Pro Ile Trp Asp Ala Ile Arg Glu Glu Ala	
65 70 75 80	
aaa ctt gag gca gag aaa gag cct att ttg agt agc ttc ttg tat gct	288
Lys Leu Glu Ala Glu Lys Glu Pro Ile Leu Ser Ser Phe Leu Tyr Ala	
85 90 95	
ggt atc tta gca cat gat tgt tta gag caa gct tta ggg ttt gtt cta	336
Gly Ile Leu Ala His Asp Cys Leu Glu Gln Ala Leu Gly Phe Val Leu	
100 105 110	
gcc aac cgt ctc caa aac cca acc ttg ttg gca aca caa ctc ttg gat	384
Ala Asn Arg Leu Gln Asn Pro Thr Leu Leu Ala Thr Gln Leu Leu Asp	
115 120 125	
ata ttt tat ggt gtt atg atg cat gac aaa ggt att cag agt tcg att	432
Ile Phe Tyr Gly Val Met Met His Asp Lys Gly Ile Gln Ser Ser Ile	
130 135 140	
cgc cat gat ctc cag gca ttt aaa gat cgt gat cct gct tgt ctg tcg	480
Arg His Asp Leu Gln Ala Phe Lys Asp Arg Asp Pro Ala Cys Leu Ser	
145 150 155 160	
tat agt tct gct att tta cat ctg aag ggt tat cat gcg tta caa gca	528
Tyr Ser Ser Ala Ile Leu His Leu Lys Gly Tyr His Ala Leu Gln Ala	
165 170 175	
tat agg gtt gcg cat aaa ctg tgg aat gaa ggg agg aaa cta tta gct	576
Tyr Arg Val Ala His Lys Leu Trp Asn Glu Gly Arg Lys Leu Leu Ala	



180	185	190	
ctt gca ttg caa agc cga ata agc gag gtt ttt ggc att gac ata cat			624
Leu Ala Leu Gln Ser Arg Ile Ser Glu Val Phe Gly Ile Asp Ile His			
195	200	205	
cca gcg gca aga att ggg gag gga ata ttg ttg gat cat gga act gga			672
Pro Ala Ala Arg Ile Gly Glu Gly Ile Leu Leu Asp His Gly Thr Gly			
210	215	220	
gtg gtc att ggt gag acc gct gtg ata ggc aac ggt gtc tcg atc tta			720
Val Val Ile Gly Glu Thr Ala Val Ile Gly Asn Gly Val Ser Ile Leu			
225	230	235	240
cat ggt gtg act tta gga gga acc gga aag gaa act ggc gat cgc cac			768
His Gly Val Thr Leu Gly Gly Thr Gly Lys Glu Thr Gly Asp Arg His			
245	250	255	
cca aag ata ggt gaa ggt gca ttg ctt gga gct tgt gtg act ata ctt			816
Pro Lys Ile Gly Glu Gly Ala Leu Leu Gly Ala Cys Val Thr Ile Leu			
260	265	270	
ggt aac ata agc ata ggt gct gga gca atg gta gct gca ggt tca ctt			864
Gly Asn Ile Ser Ile Gly Ala Gly Ala Met Val Ala Ala Gly Ser Leu			
275	280	285	
gtg tta aaa gac gtt cct tcg cat agt gtg gtg gct gga aat cct gca			912
Val Leu Lys Asp Val Pro Ser His Ser Val Val Ala Gly Asn Pro Ala			
290	295	300	
aaa ctg atc agg gtc atg gaa gag caa gac ccg tct cta gca atg aaa			960
Lys Leu Ile Arg Val Met Glu Glu Gln Asp Pro Ser Leu Ala Met Lys			
305	310	315	320
cac gat gct act aaa gag ttc ttt cga cat gta gct gat ggt tac aaa			1008
His Asp Ala Thr Lys Glu Phe Phe Arg His Val Ala Asp Gly Tyr Lys			
325	330	335	
ggg gca caa tct aac gga cca tca ctt tca gca gga gat aca gag aaa			1056
Gly Ala Gln Ser Asn Gly Pro Ser Leu Ser Ala Gly Asp Thr Glu Lys			
340	345	350	
gga cac act aac agc aca tca tga			1080
Gly His Thr Asn Ser Thr Ser			
355	360		

<210> 10

<211> 359

<212> PRT

<213> Arabidopsis thaliana

<400> 10

Met Val Asp Leu Ser Ser Phe Ser Leu Leu Phe Ala Phe Ser Val Ser  
1 5 10 15

Leu Ser Phe Val Gln Ser Lys Arg Val Cys Asp Ser Ser Leu Ser Ser  
20 25 30

Pro Trp Arg Asp Met Asn Gly Asp Glu Leu Pro Phe Glu Ser Gly Phe  
35 40 45

Glu Val Tyr Ala Lys Gly Thr His Lys Ser Glu Phe Asp Ser Asn Leu  
50 55 60

Leu Asp Pro Arg Ser Asp Pro Ile Trp Asp Ala Ile Arg Glu Glu Ala  
65 70 75 80

Lys Leu Glu Ala Glu Lys Glu Pro Ile Leu Ser Ser Phe Leu Tyr Ala  
85 90 95

Gly Ile Leu Ala His Asp Cys Leu Glu Gln Ala Leu Gly Phe Val Leu  
100 105 110

Ala Asn Arg Leu Gln Asn Pro Thr Leu Leu Ala Thr Gln Leu Leu Asp  
115 120 125

Ile Phe Tyr Gly Val Met Met His Asp Lys Gly Ile Gln Ser Ser Ile  
130 135 140

Arg His Asp Leu Gln Ala Phe Lys Asp Arg Asp Pro Ala Cys Leu Ser  
145 150 155 160

Tyr Ser Ser Ala Ile Leu His Leu Lys Gly Tyr His Ala Leu Gln Ala  
165 170 175

Tyr Arg Val Ala His Lys Leu Trp Asn Glu Gly Arg Lys Leu Leu Ala  
180 185 190

Leu Ala Leu Gln Ser Arg Ile Ser Glu Val Phe Gly Ile Asp Ile His  
195 200 205

Pro Ala Ala Arg Ile Gly Glu Gly Ile Leu Leu Asp His Gly Thr Gly  
210 215 220

Val Val Ile Gly Glu Thr Ala Val Ile Gly Asn Gly Val Ser Ile Leu

225	230	235	240
His Gly Val Thr Leu Gly Gly Thr Gly Lys Glu Thr Gly Asp Arg His			
245	250	255	
Pro Lys Ile Gly Glu Gly Ala Leu Leu Gly Ala Cys Val Thr Ile Leu			
260	265	270	
Gly Asn Ile Ser Ile Gly Ala Gly Ala Met Val Ala Ala Gly Ser Leu			
275	280	285	
Val Leu Lys Asp Val Pro Ser His Ser Val Val Ala Gly Asn Pro Ala			
290	295	300	
Lys Leu Ile Arg Val Met Glu Glu Gln Asp Pro Ser Leu Ala Met Lys			
305	310	315	320
His Asp Ala Thr Lys Glu Phe Phe Arg His Val Ala Asp Gly Tyr Lys			
325	330	335	
Gly Ala Gln Ser Asn Gly Pro Ser Leu Ser Ala Gly Asp Thr Glu Lys			
340	345	350	
Gly His Thr Asn Ser Thr Ser			
355			

<210> 11  
 <211> 900  
 <212> DNA  
 <213> Arabidopsis thaliana

<220>  
 <221> CDS  
 <222> (1)..(900)

<220>  
 <221> transit\_peptide  
 <222> (1)..(90)

<400> 11	
atg gct tgt ata aac ggc gag aat cgt gat ttt tct tcc tcg tca tct	48
Met Ala Cys Ile Asn Gly Glu Asn Arg Asp Phe Ser Ser Ser Ser Ser	
1 5 10 15	
ttg tct tct ctt cca atg att gtc tcc cgg aac ttt tct gcc aga gac	96
Leu Ser Ser Leu Pro Met Ile Val Ser Arg Asn Phe Ser Ala Arg Asp	
20 25 30	

gat gga gag acc ggt gac gag ttt cct ttc gag agg att ttc ccg gtt	144
Asp Gly Glu Thr Gly Asp Glu Phe Pro Phe Glu Arg Ile Phe Pro Val	
35 40 45	
tac gct aga gga acc ctt aat ccc gtg gcc gac ccg gtt ttg ctg gat	192
Tyr Ala Arg Gly Thr Leu Asn Pro Val Ala Asp Pro Val Leu Leu Asp	
50 55 60	
ttt acc aat tct agt tat gac cca att tgg gat tct ata aga gaa gaa	240
Phe Thr Asn Ser Ser Tyr Asp Pro Ile Trp Asp Ser Ile Arg Glu Glu	
65 70 75 80	
gct aag ctt gag gca gaa gag gag ccg gtt ttg agt agc ttc ttg tat	288
Ala Lys Leu Glu Ala Glu Glu Glu Pro Val Leu Ser Ser Phe Leu Tyr	
85 90 95	
gct agt atc ttg tcg cat gac tgt tta gag caa gca ttg agt ttt gtt	336
Ala Ser Ile Leu Ser His Asp Cys Leu Glu Gln Ala Leu Ser Phe Val	
100 105 110	
cta gct aac cgt ctc caa aac cct acc ttg ttg gca act cag ctt atg	384
Leu Ala Asn Arg Leu Gln Asn Pro Thr Leu Leu Ala Thr Gln Leu Met	
115 120 125	
gat ata ttt tgc aac gtt atg gta cat gac aga ggt att caa agc tcg	432
Asp Ile Phe Cys Asn Val Met Val His Asp Arg Gly Ile Gln Ser Ser	
130 135 140	
att cgt ctt gat gtt cag gca ttc aaa gac aga gat cct gct tgt cta	480
Ile Arg Leu Asp Val Gln Ala Phe Lys Asp Arg Asp Pro Ala Cys Leu	
145 150 155 160	
tcg tat agt tcg gct att tta cat ctg aag ggc tat ctt gca ctg cag	528
Ser Tyr Ser Ser Ala Ile Leu His Leu Lys Gly Tyr Leu Ala Leu Gln	
165 170 175	
gcg tat aga gta gca cat aag ttg tgg aag caa gga aga aaa cta tta	576
Ala Tyr Arg Val Ala His Lys Leu Trp Lys Gln Gly Arg Lys Leu Leu	
180 185 190	
gca ttg gca ctg caa agc cga gta agc gag gta aga act gct gtg ata	624
Ala Leu Ala Leu Gln Ser Arg Val Ser Glu Val Arg Thr Ala Val Ile	
195 200 205	
ggc gac cgt gtc tca att ttg cat ggt gtg aca tta gga gga act ggg	672
Gly Asp Arg Val Ser Ile Leu His Gly Val Thr Leu Gly Gly Thr Gly	
210 215 220	

aaa gaa acc ggt gac cgc cat cca aat ata ggc gac ggt gct ctt ctt 720  
 Lys Glu Thr Gly Asp Arg His Pro Asn Ile Gly Asp Gly Ala Leu Leu  
 225 230 235 240

gga gca tgt gtg act ata ctt ggt aac att aag ata ggc gct gga gca 768  
 Gly Ala Cys Val Thr Ile Leu Gly Asn Ile Lys Ile Gly Ala Gly Ala  
 245 250 255

atg gta gct gct ggt tcg ctt gtg tta aag gat gtt cct tcg cat agc 816  
 Met Val Ala Ala Gly Ser Leu Val Leu Lys Asp Val Pro Ser His Ser  
 260 265 270

atg gtg gct gga aat cca gca aaa ctc atc ggg ttt gtt gat gag caa 864  
 Met Val Ala Gly Asn Pro Ala Lys Leu Ile Gly Phe Val Asp Glu Gln  
 275 280 285

gat cca tct atg aca atg gag cat ggt gag tct tga 900  
 Asp Pro Ser Met Thr Met Glu His Gly Glu Ser  
 290 295 300

<210> 12

<211> 299

<212> PRT

<213> Arabidopsis thaliana

<400> 12

Met Ala Cys Ile Asn Gly Glu Asn Arg Asp Phe Ser Ser Ser Ser Ser  
 1 5 10 15

Leu Ser Ser Leu Pro Met Ile Val Ser Arg Asn Phe Ser Ala Arg Asp  
 20 25 30

Asp Gly Glu Thr Gly Asp Glu Phe Pro Phe Glu Arg Ile Phe Pro Val  
 35 40 45

Tyr Ala Arg Gly Thr Leu Asn Pro Val Ala Asp Pro Val Leu Leu Asp  
 50 55 60

Phe Thr Asn Ser Ser Tyr Asp Pro Ile Trp Asp Ser Ile Arg Glu Glu  
 65 70 75 80

Ala Lys Leu Glu Ala Glu Glu Glu Pro Val Leu Ser Ser Phe Leu Tyr  
 85 90 95

Ala Ser Ile Leu Ser His Asp Cys Leu Glu Gln Ala Leu Ser Phe Val  
 100 105 110

Leu Ala Asn Arg Leu Gln Asn Pro Thr Leu Leu Ala Thr Gln Leu Met  
 115 120 125  
 Asp Ile Phe Cys Asn Val Met Val His Asp Arg Gly Ile Gln Ser Ser  
 130 135 140  
 Ile Arg Leu Asp Val Gln Ala Phe Lys Asp Arg Asp Pro Ala Cys Leu  
 145 150 155 160  
 Ser Tyr Ser Ser Ala Ile Leu His Leu Lys Gly Tyr Leu Ala Leu Gln  
 165 170 175  
 Ala Tyr Arg Val Ala His Lys Leu Trp Lys Gln Gly Arg Lys Leu Leu  
 180 185 190  
 Ala Leu Ala Leu Gln Ser Arg Val Ser Glu Val Arg Thr Ala Val Ile  
 195 200 205  
 Gly Asp Arg Val Ser Ile Leu His Gly Val Thr Leu Gly Gly Thr Gly  
 210 215 220  
 Lys Glu Thr Gly Asp Arg His Pro Asn Ile Gly Asp Gly Ala Leu Leu  
 225 230 235 240  
 Gly Ala Cys Val Thr Ile Leu Gly Asn Ile Lys Ile Gly Ala Gly Ala  
 245 250 255  
 Met Val Ala Ala Gly Ser Leu Val Leu Lys Asp Val Pro Ser His Ser  
 260 265 270  
 Met Val Ala Gly Asn Pro Ala Lys Leu Ile Gly Phe Val Asp Glu Gln  
 275 280 285  
 Asp Pro Ser Met Thr Met Glu His Gly Glu Ser  
 290 295

<210> 13

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Synthetic  
Oligonucleotide

<400> 13

gagagaggat cctctttcca atcataaacc atggcaacat gcatagacac atgc

54

<210> 14

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Synthetic  
Oligonucleotide

<400> 14

ggctcaccag actaatacac taaattgtgt ttacctcgag agagag

46

<210> 15

<211> 52

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Synthetic  
Oligonucleotide

<400> 15

gagagaggat cctcttatcg ccgcgttaat atgccaccgg ccggagaact cc

52

<210> 16

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence

<400> 16

gagccttacc agtctaattgt agtatatttc aacctcgaga gagag

45

<210> 17

<211> 53

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence

<400> 17

gagagaggat cccctcctcc tcctcctcct atggctgcgt gcatcgacac ctg

53

<210> 18

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence

<400> 18

gctcaccagc ctaatacatt aaactttttc agctcgagag agag

44

<210> 19

<211> 53

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence

<220>

<223> Description of Artificial Sequence

<400> 19

gagagaggat ccggccgaga aaaaaaaaaa atgttgccgg tcacaagtcg ccg

53

<210> 20

<211> 49

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence

<400> 20

gagagaggat ccgacaagtt ggcataattt atggtggatc tatcttcct

49

<210> 21

<211> 43

<212> DNA

<213> Artificial Sequence



<220>

<223> Description of Artificial Sequence

<220>

<223> Description of Artificial Sequence

<400> 21

cctgtgtgat tgtcgtgtag tactctagaa actcgagaga gag

43

<210> 22

<211> 67

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence

<400> 22

gagagaggat ccgacaagtt ggcataattt atggcttgta taaacggcga gaatcgtgat 60

ttttctt

67

<210> 23

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence

<400> 23

tacctcgtac cactcagaac tctagaaact cgagagagag

40